

Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro  
 450 455 460

5 Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly  
 465 470 475 480

Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu  
 485 490 495

10 Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn  
 500 505 510

Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser  
 515 520 525

15 Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val  
 530 535 540

Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile  
 20 545 550 555 560

Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn  
 565 570 575

Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln  
 580 585 590

Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp  
 30 595 600 605

Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp  
 610 615 620

Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn  
 35 625 630 635 640

Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val  
 645 650 655

40 Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys  
 660 665 670

Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu  
 45 675 680 685

Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro  
 690 695 700

Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp  
 50 705 710 715 720

Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu  
 725 730 735

	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys		
	740	745	750
5	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp		
	755	760	765
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn		
	770	775	780
10	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile		
	785	790	795
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn		
	805	810	815
15	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His		
	820	825	830
20	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn		
	835	840	845
	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly		
	850	855	860
25	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu		
	865	870	875
	880		
30	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp		
	885	890	895
	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala		
	900	905	910
35	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu		
	915	920	925
	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val		
	930	935	940
40	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly		
	945	950	955
	960		
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala		
	965	970	975
45	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn		
	980	985	990
50	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu		
	995	1000	1005
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu		
	1010	1015	1020

Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg  
 1025 1030 1035 1040  
 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His  
 5 1045 1050 1055  
 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu  
 1060 1065 1070  
 10 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly  
 1075 1080 1085  
 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr  
 1090 1095 1100  
 15 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser  
 1105 1110 1115 1120  
 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys  
 20 1125 1130 1135  
 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr  
 1140 1145 1150  
 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile  
 25 1155 1160 1165  
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu  
 1170 1175 1180  
 30 Leu Leu Met Glu Glu  
 1185

35 (2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3567 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 45 (B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT  
 50 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser  
 1 5 10 15

48